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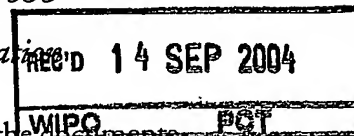
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Specification and Drawings, as originally filed, with Application for Patent Serial No:
2,432,972, on July 4, 2003, by **NATIONAL UNIVERSITY OF SINGAPORE**, assignee of
Jeak L. Ding and Bow Ho, for "Sushi Peptides, Processes for Making and Uses Thereof".

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ABSTRACT

Endotoxin, also known as lipopolysaccharides (LPS), is the major mediator of septic shock due to Gram-negative bacterial infection. Chemically synthesized S3 peptide,
5 derived from Sushi3 domain of Factor C, which is the endotoxin-sensitive serine protease of the limulus coagulation cascade, binds and neutralizes LPS activity. Fluorescent tagged-S3 is shown to detect LPS-containing bacteria. For large-scale production of S3 and to mimick
10 other pathogen-recognizing molecules, tandem multimers of the S3 gene were constructed and expressed in *E. coli*. Tetramer of S3 is shown to display an enhanced inhibitory effect on LPS-induced activities. An affinity matrix bases on tetramer of S3 is also shown to be particularly efficient
15 at removing LPS.

SUSHI PEPTIDES, PROCESSES FOR MAKING AND USES THEREOF

BACKGROUND

Sepsis remains a leading cause of death in critical care unit, and is also frequently associated with serious consequence such as multiple organ failure. Gram-negative bacterial endotoxin, also known as lipopolysaccharide (LPS), has been suggested to play a pivotal role in such septic complications (Houdijk et al, 1997). The acute phase plasma protein, LPS binding protein (LBP), binds circulating LPS to extract it from micelles, and transfer it to either soluble or membrane-bound CD14 receptor in monocytes and macrophages. The interaction of this complex with Toll-like receptors (TLRs) is thought to initiate intracellular signaling reactions, via transcription factor NF- κ B (Ulevitch et al, 1999). Activation of protein kinases mediates the production of inflammatory cytokines, which contribute to septic shock. It has also been shown that in the absence of plasma LBP, the LPS is able to directly interact with CD14, yielding similar effects (Wyckoff et al, 1998). Thus, treatment of endotoxaemia and sepsis would be greatly aided by blocking the activity of endotoxin and/or removing them from the body fluids of patients, as cationic peptides and synthetic analogues do (de Haas et al, 1998; Scott et al, 2000).

LPS from gram-negative bacteria induces the amoebocytes of limulus to aggregate and degranulate. This response underlies the important defense mechanism of limulus against invasion of gram-negative bacteria (Ding et al, 1995). As a molecular biosensor, Factor C can be autocatalytically activated by femtograms of LPS to trigger the coagulation cascade (Ho, 1983), suggesting that it contains high affinity LPS-binding domains. Recently, two

regions of Factor C that exhibit exceptionally high LPS binding affinity were defined as the Sush11 and Sush13 domains (Tan et al, 2000a). Two 34-mer synthetic peptides, S1 and S3, spanning the 171-204 and 268-301 amino acid residues of Factor C (GenBank Accession No. S77063), are derived from Sush11 and Sush13 domains, respectively. Both peptides inhibit LPS-induced limulus amoebocyte lysate (LAL) reaction and LPS-induced hTNF- α secretion (Tan et al, 2000b). See also US09/626,795, the entire content of which is herein incorporated by reference. The application value of these two peptides would be boosted if they could be obtained by cost effective and large-scale methods such as recombinant expression in prokaryotic systems. However, expression of smaller peptides tends to encounter technical difficulties (Le et al, 1991; Latham,1999).

Trace levels of endotoxin or lipopolysaccharides (LPS) cause pathophysiological reactions such as fever, changes in white blood cell counts, disseminated intravascular coagulation, hypotension, shock and death. Intensive research is being carried out to develop more sensitive techniques that are able to remove minute levels of endotoxin from pharmaceutical fluids to meet higher standards of safety (Petsch 2000). Adsorption methods have proven to be the most effective (Minobe 1982) in removing endotoxins from solutions and many methods have been developed for different target solutions with varying efficiencies. However, most of these methods are not efficient over a wide range of pH and ionic strength (Petsch 2000). In addition, there is always a compromise between protein recovery and LPS removal, such that the clearance factor is often disappointing when the LPS feed concentration is low.

SUMMARY OF THE INVENTION

In one aspect, there is described a polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3.

5

In another aspect, there is described S3 peptide tagged with a detectable label.

10 In another aspect, there is described a method of producing the polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3, the method comprising the steps of expressing a multimer of S3 in a host cell and cleaving the multimer of S3. The method may further comprise the step of isolating the tetrameric repeat
15 from S3 monomer or non-tetrameric S3. Cleavage may be effected, though not restricted to, acid digestion or proteolytic digestion.

In another aspect, there is described a method for
20 detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3, and detecting binding between LPS and the polypeptide comprising a
25 tetrameric repeat of S3, or consisting of a tetrameric repeat of S3.

In another aspect, there is described a method for detecting LPS-containing bacteria comprising the step of
30 contacting a sample containing LPS-containing bacteria with the polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3, and detecting inhibition of LPS-induced activity.

In another aspect, there is described a method for treating endotoxaemia or sepsis comprising the step of administering the polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3 to a
5 patient suffering from endotoxaemia or sepsis.

In another aspect, there is described a method for detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with
10 the polypeptide of S3 peptide tagged with a detectable label, and detecting binding between LPS and S3 peptide tagged with the detectable label.

In another aspect, there is described a method for
15 detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with S3 peptide tagged with a detectable label, and detecting inhibition of LPS-induced activity.

20 In another aspect, there is described a method for detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide of S3 peptide tagged with a fluorescence label, and detecting bacteria-associated fluorescence from
25 the label.

In another aspect, there is described a polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3, or S3 peptide,
30 immobilized on a solid medium such as agarose bead.

In another aspect, there is described a method for removing LPS or LPS-containing bacteria from a sample,

comprising the step of contacting the sample with the immobilized polypeptide comprising a tetrameric repeat of S3, or consisting of a tetrameric repeat of S3, or S3 peptide, under conditions which allow binding of LPS-containing bacteria to the immobilized polypeptide, wherein unbound material is substantially free of LPS or LPS-containing bacteria.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a schematic representation of the multimerization of S3 gene using the gene amplification vector, pBC. The *BbsI* site was introduced into the S3 primers, and the amplified gene was cloned into pBC vector. After the *BbsI* digestion, the S3 gene with overhang terminals were self-ligated at 16 °C for 2 h, and inserted into pBC which was previously linearised with *BbsI*. The CCCC head motif on the sense strand and GGGG tail motif on anti-sense strand allowed the fragments to self-ligate directionally, giving rise to multimers of pBCS3-nMer constructs. These multimeric inserts were subsequently released and recloned into expression vector pET22b.

Figure 2 shows an identification of multimers of S3 gene and expression in *E. coli*. (a) Electrophoretic analysis of the multimeric S3 genes. The number of S3 inserts cloned in the pBC was determined by digestion with *NdeI* and *HindIII*, which flank the multimers. The digests were resolved on 2 % agarose gel. Lane M, 100 bp DNA ladder; lanes 1-4, *NdeI* and *HindIII* digested pBCS3-1, -2, -4, -8mer, which contain 1, 2, 4, 8 copies of S3 gene. (b) Expression of multimers of S3 gene in *E. coli* BL21. The recombinant peptides were resolved on SDS-PAGE constituting 5 % stacking gel and 18 % resolving gel. Lane M, peptide markers; lane 1, BL21 containing pET22b; lanes 2-5, BL21

containing S3-1, -2, -4, -8mer, respectively; lane 6, purified rS3-4mer. The arrows indicate the recombinant proteins.

Figure 3 shows a time course of formic acid cleavage of rS3-4mer into monomers and Western blot analysis of recombinant peptides. (a) Digestion of rS3-4mer into monomers. The rS3-4mer was dissolved in cleavage buffer and incubated at 42 °C with constant and gentle shaking. At 12, 24, 36 and 48 h, aliquots of 100 µl of samples were sampled and added to 900 µl of ethanol, chilled at -20 °C for 30 min, centrifuged at 15000g for 10 min, and dissolved in loading buffer for electrophoretic resolution on tricine SDS-PAGE with 5 % stacking gel and 15 % resolving gel. Lanes 1-4 are samples digested for 12, 24, 36, 48 h, respectively; lane 5, intact rS3-4mer. (b) Western blot analysis of recombinant peptides. Lane 1, total expressed cell proteins. The expressed 18.4 kDa rS3-4mer strongly reacts with anti-S3 antibody; lane2, partially digested peptide mixtures containing rS3-1, -2, -3, -4mer ; lane 3, rS3-1mer derived from the rS3-4mer; lane 4, synthetic S3 peptide. All peptides derived from rS3-4mer reacted with the antibody.

Figure 4 shows an ELISA-based LPS binding assay. LPS was coated overnight on 96-well plates. Varying concentrations of peptides were allowed to interact with the immobilized LPS. The amount of bound peptides was determined by rabbit anti-S3 IgG and quantitated by ABTS substrate. The average OD_{405nm} of the triplicate samples were calculated and plotted with the corresponding concentration.

Figure 5 shows a comparison of rS3-4mer and -1mer with synthetic S3 in inhibition of LPS-induced LAL assay and hTNF-α secretion in human THP-1 cells. (a) Inhibition of

LPS-induced LAL assay. Binding of the peptides to LPS would competitively inhibit the chromogenic reaction in kinetic-QCL LAL test. The ENC_{50} values of rS3-4, rS3-1mer and synthetic S3 peptide were determined to be 5.4 $\mu\text{g/ml}$, 9.2 $\mu\text{g/ml}$, 10.2 $\mu\text{g/ml}$, respectively. (b) Suppression of LPS-induced hTNF- α secretion in human THP-1 cells. The rS3-4mer and rS3-1mer were tested for their ability to suppress LPS-induced hTNF- α secretion from THP.1 cells. Both peptides inhibit hTNF- α production in a dose-dependent manner, albeit with different efficiency. rS3-4mer required only 40.4 $\mu\text{g/ml}$ to achieve ENC_{50} , compared to 83.2 $\mu\text{g/ml}$ needed for rS3-1mer. The decrease in TNF- α secretion was expressed as percentage of control (LPS only).

DETAILED DESCRIPTION OF EMBODIMENTS

S3 has been shown to be one of the LPS-binding sites of Factor C, and is able to suppress the LPS-induced cytokine production in macrophages (Tan et al, 2000b). The immobilized S3 peptide analogue can remove LPS from culture medium with high efficiency (Ding et al, 2001). Thus, this promising reagent can be applied to prevent sepsis due to circulating LPS, which is released by viable or injured Gram-negative bacteria. Chemical synthesis is an uneconomical approach to obtain large quantity of this peptide, whereas expression in *E. coli* may be more cost-effective (Latham, 1999). However, the yield from *E. coli* may be low and unstable (Le et al, 1991). Thus, expression of the multimers of peptides would circumvent the abovementioned problems (Kajino et al, 2000). A more important attribute for recombinant multimers of S3 is the expected enhancement in ligand-binding affinity and LPS-neutralisation activity achieved through synergistic effects

of multiple LPS-binding units in one molecule (Mauro et al, 2000).

Many methods can be applied to construct the tandem repeats of a peptide (Lee et al, 2000; Mauro, et al, 2000; Dolby, et al, 1999). In one embodiment, we chose the amplification vector that readily allows us to obtain various multimers of S3 gene. Furthermore, we designed the DP linker between the repetitive units, to afford convenient cleavage under mildly acidic buffer to release the monomers.

Studying the tandem repeats of S3 may provide explanations as to why some proteins adopt repetitive structure, and how they contribute strategically towards pathogen recognition. In one embodiment, tandem repeats of S3 gene were cloned into a modified vector, which was subsequently transferred to an expression vector, pET22b. Induced expression of the most robust tetramer clone was scaled-up. Recombinant S3 tetramer (rS3-4mer) was purified and digested into monomers (rS3-1mer) by acid treatment, and both the recombinant peptides were tested for their endotoxin binding and neutralizing activities.

The multimeric constructs exhibit different expression levels. No expression was observed with the pETS3-1mer. As the copy number increases, the expression level improved dramatically, especially with the S3 tetramer, where the expression level reached 25 % of the total cell proteins. However, further doubling to 8mer reduced the expression level, suggesting that the copy number is not always proportional to the expression level for this peptide. The ELISA-based LPS binding test and SPR result show differential binding efficiencies of rS3-4mer, rS3-1mer and the synthetic S3 for LPS, with highest binding achieved by rS3-4mer. Both the LAL inhibition test and

suppression of TNF- α release in THP-1 cells showed that rS3-1mer works equally well as the synthetic S3 peptide to neutralize LPS, while rS3-4mer displayed a 2-fold higher anti-LPS activity. However, the rS3-1mer and synthetic S3 showed inconsistent results in ELISA and SPR tests.

Two major forces mediate the interaction between LPS and LPS-binding peptides. The positive charge on the peptides forms an electrostatic attraction with the negatively charged phosphate head groups of the LPS. The other is the hydrophobic interaction between them (Goh et al, 2002; Farley et al, 1988). In fact, mutation of amino acid residues of S3 aimed at introducing positive charges only achieved a slight increase in LPS-neutralizing activity (Tan et al, 2000b). Besides charge modification, little effort has been taken to enhance the LPS-binding ability of such peptides. Herein, by creating tandem repeats of the LPS-binding units instead of increasing the number of positive charges, we demonstrate a 2-fold improvement in activity of the tetramer compared to the original monomeric unit, thus providing an alternative strategy to improve the LPS-binding activity of similar peptides.

The result of secondary structure analysis by DNAMAN program (Version 4.15, Lynnon Biosoft) shows that both S1 and S3 have a distinctive structure of four regular β -sheets alternately spaced by turns and coils. We presume that this structure may be important to the interaction with LPS, and in addition, the multiple β -sheets in rS3-4mer, may form the β -barrel structure to provide better shielding of hydrophobic acyl chain of LPS (Ferguson et al, 1998).

We have developed a specific endotoxin adsorption using rS3-4mer, which is a recombinant tetramer of S3. Its high binding affinity of LPS, lower cytotoxicity and

haemolytic activity showed its advantage over the synthetic amphipathic cationic peptide, S3A. rS3-4mer was covalently conjugated to DADPA immobilized agarose. The efficacy of this matrix to remove LPS was tested under different
5 conditions and compared with the S3A matrix.

Compared to S3A synthetic peptide, the rS3-4mer recombinant peptide appears to be on par if not better in terms of efficiency of LPS removal. The tandem repeats of the S3 might expose strategically positioned multiple LPS-
10 binding motifs, which produce synergistic effect for binding LPS. Both of these peptides have great potential for the pyrogen clean-up industry, as they are re-usable, non-toxic and efficient in removing trace amounts of LPS from solutions. Better systems of removing LPS from solutions
15 will be required to meet demands of new and tighter legislations.

Before describing the present invention in further detail, it is to be understood that this invention is not limited to particular formulations or process parameters as
20 such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments of the invention only, and is not intended to be limiting.

Although a number of compositions and methods
25 similar or equivalent to those described herein can be used in the practice of the present invention, the preferred materials and methods are described herein.

In one aspect, the invention encompasses (i) an expression cassette containing a DNA molecule of the
30 invention placed under the control of the elements required for expression, in particular under the control of an

appropriate promoter; (ii) an expression vector containing an expression cassette of the invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well
5 as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow
10 expression of the DNA molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture. It is understood that by the term "polypeptide" includes short amino acid sequences commonly termed "peptides".

15 A recombinant expression system is selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (e.g., COS1, NIH3T3, or JEG3 cells), arthropods cells (e.g., *Spodoptera frugiperda* (SF9)
20 cells), and plant cells. A preferred expression system is a procaryotic host such as *E. coli*. Bacterial and eucaryotic cells are available from a number of different sources including commercial sources to those skilled in the art, e.g., the American Type Culture Collection (ATCC; Rockville,
25 Maryland). Commercial sources of cells used for recombinant protein expression also provide instructions for usage of the cells.

The choice of the expression system depends on the features desired for the expressed polypeptide. For
30 example, it may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form.

One skilled in the art would readily understand that not all vectors and expression control sequences and hosts would be expected to express equally well the polynucleotides of this invention. With the guidelines
5 described below, however, a selection of vectors, expression control sequences and hosts may be made without undue experimentation and without departing from the scope of this invention.

In selecting a vector, the host must be chosen
10 that is compatible with the vector which is to exist and possibly replicate in it. Considerations are made with respect to the vector copy number, the ability to control the copy number, expression of other proteins such as antibiotic resistance. In selecting an expression control
15 sequence, a number of variables are considered. Among the important variable are the relative strength of the sequence (e.g. the ability to drive expression under various conditions), the ability to control the sequence's function, compatibility between the polynucleotide to be expressed and
20 the control sequence (e.g. secondary structures are considered to avoid hairpin structures which prevent efficient transcription). In selecting the host, unicellular hosts are selected which are compatible with the selected vector, tolerant of any possible toxic effects of
25 the expressed product, able to secrete the expressed product efficiently if such is desired, to be able to express the product in the desired conformation, to be easily scaled up, and to which ease of purification of the final product.

The choice of the expression cassette depends on
30 the host system selected as well as the features desired for the expressed polypeptide. Typically, an expression cassette includes a promoter that is functional in the

selected host system and can be constitutive or inducible; a ribosome binding site; a start codon (ATG) if necessary; a region encoding a signal peptide, e.g., a lipidation signal peptide; a DNA molecule of the invention; a stop codon; and optionally a 3' terminal region (translation and/or transcription terminator). The signal peptide encoding region is adjacent to the polynucleotide of the invention and placed in proper reading frame. The signal peptide-encoding region is homologous or heterologous to the DNA molecule encoding the mature polypeptide and is compatible with the secretion apparatus of the host used for expression. The open reading frame constituted by the DNA molecule of the invention, solely or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter araB) and is functional in Gram-negative bacteria such as *E. coli* (as described in U.S. Patent No. 5,028,530 and in Cagnon et al., (Cagnon et al., Protein Engineering (1991) 4(7):843)); the promoter of the gene of bacteriophage T7 encoding RNA polymerase, that is functional in a number of *E. coli* strains expressing T7 polymerase (described in U.S. Patent No. 4,952,496); OspA lipidation signal peptide; and RlpB lipidation signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (e.g., plasmids or viral vectors) can be chosen, for example, from those described in Pouwels et al. (Cloning

Vectors: A Laboratory Manual 1985, Supp. 1987). Suitable expression vectors can be purchased from various commercial sources.

Methods for transforming/transfecting host cells
5 with expression vectors are well-known in the art and depend on the host system selected as described in Ausubel et al., (Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994).

Upon expression, a recombinant polypeptide of the
10 invention (or a polypeptide derivative) is produced and remains in the intracellular compartment, is secreted/excreted in the extracellular medium or in the periplasmic space, or is embedded in the cellular membrane. The polypeptide is recovered in a substantially purified form
15 from the cell extract or from the supernatant after centrifugation of the recombinant cell culture. The recombinant polypeptide is purified by any well-known methods that can be readily adapted by a person skilled in the art, such as fusion of the polynucleotide encoding the
20 polypeptide or its derivative to a small affinity binding domain.

In various embodiments, a polypeptide may be cleaved to obtain the desired multimer or monomer. Proteolytic cleavage can be done by methods known in the
25 art. One method may be acid digestion. Alternatively, a proteolytic cleavage site may be introduced at the junction of the fission moiety so that the desired peptide can ultimately be separated from the remainder of the polypeptide. Proteolytic enzymes include, but are not
30 limited to, factor Xa, thrombin, and enterokinase.

By "S3 multimer" is meant a molecule having more than one copy of S3 peptide, or multiple tandem repeats of S3 peptide. The S3 peptide sequences may all be the same, or may correspond to different derivatives, analogs, 5 variants of S3 so long as they retain the ability to bind to LPS. If the S3 peptides are linked either chemically or recombinantly to a carrier, they may be linked to either the 5'-end, the 3'-end, or may flank the carrier in question. Further, the S3 multimer may be located at sites internal to 10 the carrier.

Spacer sequences may be present between the S3 moieties. The strategic placement of various spacer sequences between S3 sequences can be used to confer even greater LPS-binding. Accordingly, under the invention, a 15 selected spacer sequence may encode a wide variety of moieties such as a single amino acid linker or a sequence of two to several amino acids. Selected spacer groups may preferably provide enzyme cleavage sites so that the expressed multimer can be processed by proteolytic enzymes 20 in vivo (by APCs, or the like).

In various embodiments, a peptide may be labeled. The peptides may be labeled at any position in the amino acid sequence, such as at the N-termini, C-termini, or at an amino acid side chain (e.g., Lys, Arg, Ser, Cys, Tyr, Glu, 25 Asp, etc.). However, since not all side chains will be present in all of the peptides produced in the digest, labeling at the N-, or C-termini is preferred. N-terminal peptide labeling is particularly preferred.

Preferred labeling groups are fluorescent 30 chromophores that are conventionally used as reporter groups. For example, the structurally related cyanine (Cy.TM.) fluorescent labeling reagents, Cy3 and Cy5, may be

used to produce N-terminally-tagged peptides. Incubation of the Cy3 or Cy5 monofunctional succinimide esters with the peptide will result in N-terminal labeling of the peptides. These dyes are commercially available from Amersham

5 Pharmacia Biotech.

AlexaTM dyes marketed by Molecular Probes, Inc. may also be used. These dyes comprise a series of fluorophores with emission maxima throughout the visible spectrum. Of these, two dyes, Alexa 532 and Alexa 568 would be especially
10 suitable. Both share a similar fluorophore and bear the same polar sulfonate and quaternary nitrogen functional groups in similar spatial orientation in the molecule. Their emission maxima are at 554 nm and 603 nm, respectively.

A variety of techniques well-known for separating
15 peptides may be used to separate and detect the peptides and their multimers. For example, such techniques include 2D gel electrophoresis, capillary electrophoresis, isoelectric focusing and liquid chromatography, and high-performance liquid chromatography (HPLC). Reverse-phase HPLC is a
20 routine analytical procedure in the field of protein and peptide analysis.

In reverse phase HPLC C-18 columns typically are used, although shorter-chain stationary phases provide improved resolution for larger polypeptides. Three column
25 formats are most widely used. Analytical columns (4.6 mm I.D.) typically are eluted at flow rates of 0.5-2 mL min⁻¹. Narrow bore columns (1 mm I.D.) are run at approximately 0.1 mL min⁻¹. Fused silica capillary columns (0.1-0.3 mm I.D.) are eluted a flow rates of 4μL min⁻¹ and below.

30 In various embodiments, the polypeptides of the invention may be immobilized on solid phase media.

Generally, the matrix provides a scaffold which allows the polypeptide to which it is linked to be separated from the bulk fluid. Non-limiting examples of suitable matrices include: polymers which are insoluble in water or mixtures
5 of water and water soluble organic solvents; beaded supports such as magnetic beads, chromatographic packing supports, media and resins; porous beaded supports such as chromatographic packing supports, media and resins (e.g. anion exchange chromatography media), a cast polymer such as
10 a membrane (e.g. polyvinylidene difluoride, Teflon, polyethylene, polypropylene or polysulfone); co-polymeric materials and gels (e.g. polyacrylamide or agarose).

In various embodiments, the polypeptides of the invention may be used therapeutically in formulations or
15 medicaments to prevent or treat sepsis-related disease. The invention provides corresponding methods of medical treatment, in which a therapeutic dose is administered in a pharmacologically acceptable formulation, e.g. to a patient or subject in need thereof. Accordingly, the invention also
20 provides therapeutic compositions comprising the polypeptide of the invention, and a pharmacologically acceptable excipient or carrier. In one embodiment, such compositions include the polypeptide of the invention in a therapeutically or prophylactically effective amount
25 sufficient to treat sepsis-related conditions. The therapeutic composition may be soluble in an aqueous solution at a physiologically acceptable pH.

A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time
30 necessary, to achieve the desired therapeutic result, such as a reduction of symptoms related to sepsis and in turn a reduction in sepsis-related disease progression. A

therapeutically effective amount of the polypeptide of the invention may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the compound to elicit a desired response in the individual. Dosage regimens may be adjusted to provide the optimum therapeutic response. A therapeutically effective amount is also one in which any toxic or detrimental effects of the compound are outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result, such as preventing or inhibiting the rate of sepsis onset or progression. A prophylactically effective amount can be determined as described above for the therapeutically effective amount. For any particular subject, specific dosage regimens may be adjusted over time according to the individual need and the professional judgement of the person administering or supervising the administration of the compositions.

As used herein "pharmaceutically acceptable carrier" or "excipient" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. In one embodiment, the carrier is suitable for parenteral administration. Alternatively, the carrier can be suitable for intravenous, intraperitoneal, intramuscular, sublingual or oral administration. Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional

media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions of the invention is contemplated. Supplementary active compounds can also be incorporated into the compositions.

5 Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration. The carrier can be a solvent or
10 dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance
15 of the required particle size in the case of dispersion and by the use of surfactants. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable
20 compositions can be brought about by including in the composition an agent which delays absorption, for example, monostearate salts and gelatin. Moreover, the polypeptide of the invention can be administered in a time release formulation, for example in a composition which includes a
25 slow release polymer. The active compounds can be prepared with carriers that will protect the compound against rapid release, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as
30 ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid and polylactic, polyglycolic copolymers (PLG). Many methods for the

preparation of such formulations are patented or generally known to those skilled in the art.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g. the polypeptide of the invention) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. In accordance with an alternative aspect of the invention, the polypeptide of the invention may be formulated with one or more additional compounds that enhance the solubility of the polypeptide.

In accordance with another aspect of the invention, therapeutic compositions of the present invention, comprising the polypeptide of the invention, may be provided in containers or commercial packages which further comprise instructions for use of the polypeptide of the invention, in the prevention and/or treatment of sepsis-related disease, or for the preparation of a medicament for prevention and/or treatment of sepsis-related disease.

EXAMPLES

LPS from *Escherichia coli* 055:B5 was purchased from Sigma (St. Louis, MO.). LAL kinetic-QCL kit was supplied by BioWhittaker (Walkersville, MD). Human TNF- α kit

(OptEIA ELISA) was from Pharmingen (San Diego, CA).

CellTiter 96 Aqueous One Solution Reagent for cytotoxicity assay was purchased from Promega (Madison, WI). Enzymes for DNA manipulation and polymerase reactions were purchased
5 from NEB (Beverly, MA.). DNA purification and extraction kits were from Qiagen (Chatsworth, CA). Pyrogen-free water for making buffers was from Baxter (Morton Grove, IL).

rS3-4mer is a tetramer with tandem repeat of the S3 gene. An endotoxin removing affinity matrix was developed
10 by using 1-ethyl-3- (3- dimethylaminopropyl) carbodiimide (EDC) as a coupling agent to link rS3-4mer to DADPA-immobilized agarose gel (Pierce, USA). The rationale for choosing DADPA-immobilized agarose matrix is based on reference (Ding et al. 2001). The LAL Kinetic-QCL assay kit
15 was from BioWhittaker, USA. LPS (*Escherichia coli* 055:B5) and sodium deoxycholate (DOC) were from Sigma. RPMI 1640 was from Gibco, BRL. Chymotrypsinogen A was purchased from Pharmacia Biotech. All other chemicals were of analytical grade from Sigma.

20 All materials relating to the affinity matrix studies were depyrogenated. Glassware and sodium chloride were baked at 200°C for 4 hours. Sterile disposables were used whenever possible and were autoclaved at 121°C for 2 hours before use. All solutions and buffers were prepared
25 using pyrogen-free water. LPS was sonicated for 5 minutes in a 37°C water bath prior to use, to disperse the aggregates.

(1) Construction of multimers of S3 gene

Using a cloned Factor C Sushi3 domain, pAC5.1Sushi3EGFP (Tan et al, 2000), the LPS-binding motif,
30 S3, was amplified by PCR. A cloning strategy, which allows for directional multimerization and cloning is shown in

Figure 1. Briefly, the amplification vector pBBSI (Lee et al, 1997) was modified to include an *NdeI* site containing the start codon adjacent to *BbsI* site. This modified vector was named pBC. Forward primer: 5'-

5 TCGAAGACGGCCCCAGGATCCCCATGCTGAACACAAGG-3' was designed with *BbsI* restriction site (GAAGAC) followed by GGCCCC in addition to the S3 flanking sequence. On the reverse primer: 5'TAGAAGACCCGGGGTCCATCAAAGAAAGTAGTTA-3', similar motif was also introduced. Digestion of the PCR product by
 10 *BbsI* would yield fragments with complementary overhang of CCCC on the sense strand and GGGG on the antisense strand, which can be used for directional multimerization and cloning. In addition, GATCCC sequence, which codes for aspartate (D) and proline (P), was introduced into the
 15 forward primer. The peptide bond between D and P can be cleaved under acidic condition (Szoka et al, 1986), thus releasing single S3 units from the recombinant multimers. In this case, the PCR products of S3 were cloned into pBC vector, and the S3 gene was released by *BbsI* digestion and
 20 allowed to self-ligate first, before cloning into the pBC vector, which was previously linearised with *BbsI*. The multimers of S3 gene were selected and identified by enzyme digestion and sequencing.

(2) Expression of the multimers of S3 gene in *E. coli*

25 To construct expression vectors bearing tandem S3 genes under the control of T7 promoter, the fragments flanked by *NdeI* and *HindIII* (containing the multimeric S3 genes) were cloned into the vector pET22b, previously linearised with *NdeI* and *HindIII*. The constructs were
 30 transformed into *E. coli* host, BL21 (DE3) for expression. The colonies were cultured overnight in LB medium with 100 µg /ml ampicillin at 37 °C, then diluted 1:100 into fresh LB

medium with 100 µg/ml ampicillin and grown to OD_{600nm} of 0.6 before induction with 0.5 mM IPTG (Promega). The cells were harvested every h up to 12 h, and the expressed products were monitored by SDS-PAGE.

5 (3) *Solubilization of inclusion bodies and purification of rS3-4mer*

One litre cultures were pelleted at 5000g for 10 min at 4 °C and resuspended in 60 ml of lysis buffer containing 20 mM Tris-Cl, pH 8.0 and 0.5 mM DTT. The
10 bacterial cells in the suspension were passed through French Press (Basic Z 0.75KW Benchtop Cell Disruptor, UK) operated at 15 kpsi, for 4 rounds in order to generate > 90 % cell disruption. The inclusion bodies were recovered by centrifugation at 12000g for 20 min at 4 °C and washed with
15 20 mM Tris-Cl buffer containing 1 M urea and 0.5 % Triton X-100. The inclusion bodies were denatured and solubilized in 20 mM Tris-Cl with 8 M urea at room temperature for 2 h. Insoluble materials were removed by centrifugation at 16000g for 20 min, and the supernatant was filtered and purified by
20 anion exchange using ÄKTA explorer (Pharmacia). Briefly, 30 ml of solubilized proteins were applied to a Q-Sepharose column (26 mm x 300 mm) equilibrated with buffer A (4 M urea, 20 mM Tris-Cl, pH 6.7). After washing with 4 column volumes of buffer A, the proteins were eluted with a linear
25 gradient of 0 % to 30 % buffer B (4 M urea, 20 mM Tris-Cl, pH6.7, 1 M NaCl) and the fractions were collected for SDS-PAGE analysis. The collected fractions were pooled and dialyzed in 10 kDa molecular weight cut-off (MWCO) pore size dialysis tubing (Snakeskin, Pierce), against refolding
30 buffer A containing 50 mM glycine, pH 9.5, 10 % sucrose, 1 mM EDTA, 2 M urea, at 4 °C for 16 h, followed by buffer B

containing 20 mM diethanolamine, pH 9.5, 10% (w/v) sucrose, 1 mM EDTA, 4 °C for another 8 h.

(4) *Monomerization of rS3-4mer into rS3-1mer by acid digestion*

5 Two adjacent amino acids, aspartate and proline were added between the S3 units, so as to act as cleavable DP linkers. The renatured rS3-4mer was precipitated with 9 volumes of ethanol, frozen at -80 °C for 1 h or at -20 °C overnight. The mixture was centrifuged at 16000g for 10 min
10 and the pellet was washed with 90 % ethanol, dried, dissolved in digestion buffer (70 % formic acid, 6 M guanidine-Cl) and digested at 42 °C for 72 h. The final products were subjected to ethanol precipitation and dissolved in 20 mM Tris-Cl pH 7.3. The cleaved rS3 peptides
15 were then dialyzed overnight against the same buffer using dialysis tubing of 1.5 kDa MWCO pore size (Sigma), thus removing the small linkers and residual salt. The endotoxin contaminant in rS3-4mer and rS3-1mer was removed by Triton X-114 phase separation (Liu et al, 1997) followed by
20 polymyxin B affinity chromatography (Detoxi-Gel™, Pierce).

Tricine SDS-PAGE and Western blot analysis: The recombinant proteins were resolved on tricine SDS-PAGE, using 5 % stacking gel and 15 % separating gel, and detected by Coomassie blue staining (Schagger et al, 1987). Western
25 analysis was performed according to the manufacturer's instruction, using ECL Western analysis system (Pierce, IL). The blot was probed with polyclonal rabbit anti-S3 antibody followed by goat anti-rabbit secondary antibody conjugated to horseradish peroxidase, HRP (DAKO, CA). The blots were
30 visualised using Supersignal West Pico Chemiluminescent Substrate and exposed to X-ray film.

(5) Assays for LPS-neutralizing activity

(a) ELISA-based LPS binding assay

The polysorp 96-well plate (MaxiSorp™, Nunc) was first coated with 100 µl per well of 4 µg/ml (approximately 5 1 µM) of LPS diluted in pyrogen-free phosphate-buffered saline (PBS). The plate was sealed and incubated overnight at room temperature. The wells were aspirated and washed 4 times with 300 µl wash solution (PBS containing 0.05 % Tween-20). The wells were blocked with wash solution 10 containing 2 % BSA for 1 h at room temperature. After washing 2 times, varying concentrations of peptides were allowed to interact with bound LPS at room temperature for 3 h. Bound peptides were detected by incubation with rabbit anti-S3 antibody and 1:2000 of goat anti-rabbit antibody 15 conjugated with HRP. Each antibody was incubated for 2 h at 37 °C. In the final step, 100 µl of substrate, ABTS (Boehringer Mannheim), was added. The absorbance was measured at 405nm with reference wavelength at 490nm.

(b) Endotoxin neutralization assay based on anti-LAL test

20 The LAL Kinetic-QCL kit utilizes the initial part of the LPS-triggered cascade in limulus amoebocyte lysate to achieve an enzymatic reaction, which catalyses the release of p-nitroaniline from a synthetic substrate, producing a yellow color, which is quantifiable by absorbance at 405_{nm}. 25 The ENC₅₀ (Endotoxin Neutralization Concentration) refers to the peptide concentration required to neutralize 50 % of a predetermined quantity of endotoxin. A low ENC₅₀ indicates high potency of the peptide for endotoxin neutralization.

In this assay, peptides of different 30 concentrations were incubated for 1 h at 37 °C with or

without an equal volume of LPS in disposable, endotoxin-free borosilicate tubes. Fifty microliters of each mixture was then dispensed into wells of a sterile microtiter plate (Nunclon™ Δsurface, Nunc). Fifty microliters of freshly reconstituted LAL reagent was dispensed into each well. The absorbance at 405_{nm} of each well was monitored after 45 min, and the concentration of peptides corresponding to 50 % inhibition of LAL activity was designated ENC₅₀.

(6) *Suppression of LPS-induced hTNF-α secretion in human*

10 *THP-1 cells*

THP-1 cells were cultured at 37 °C in a humidified environment in the presence of 5 % CO₂. RPMI 1640 medium was supplemented with 10 % fetal bovine serum (FBS), penicillin (100 U/ml), and streptomycin (100 µg/ml). The cells were maintained at a density of 2.5×10⁵⁻⁶ cells/ml. THP-1 monocytes were transformed into macrophages by addition of phorbol myristic acid, PMA (Sigma) at a stock of 0.3 mg/ml in dimethyl sulfoxide to give a final concentration of 30 ng/ml and 0.01 % dimethyl sulfoxide. PMA-treated cell suspensions were immediately plated into 96-well microtiter plate at a density of 4×10⁵ cells/ml and allowed to differentiate for 48 h at 37 °C. The culture medium was removed and the cells were washed twice with serum-free RPMI 1640. Thereafter, the macrophages were stimulated with 50 EU/ml LPS (a specific activity of LPS that has been standardized by LAL test against FDA-approved LPS standards), peptides alone or LPS (preincubated with various concentrations of peptides) and incubated at 37 °C. After 6 h, the culture medium was collected and hTNF-α concentration in the supernatants was assayed using ELISA.

(7) *Realtime interaction analysis between peptides and LPS*

Surface plasmon resonance (SPR) analysis of the real time interaction between peptides and LPS was performed with BIAcore 2000 (Pharmacia) using HPA chip (Tan et al, 2000b). The affinity constant was calculated using BIAevaluation software 3.0. The mean values were obtained from three independent experiments.

(8) *Cytotoxicity of peptides in eukaryotic cells*

THP-1 monocytes in 50 μ l of 2×10^4 cells/ml in RPMI 1640 were mixed in a microtiter plate with 50 μ l of two-fold serial dilutions of peptides ranging in concentration, and incubated for 60 min at 37 °C. To determine the cytotoxicity induced by the peptides, 20 μ l of CellTiter 96 Aqueous One Solution Reagent was added into each well for 90 min at 37 °C. MTS [3-(4, 5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium] is bio-reduced by metabolically active cells into a colored formazan product that is soluble in tissue culture medium. For detection, the absorbance was measured at 490_{nm}. To determine the ratio of cell lysis induced by the peptides, two controls were included by incubating cells in PBS containing 0.2 % Tween-20 instead of medium only. This absorbance value corresponds to the background, as those cells could not metabolize MTS.

(9) *Data Analysis of S3 Tandem Repeats Studies*

Recombinant expression of S3 tandem repeats, purification and cleavage to monomers

A 143 bp S3 gene fragment was obtained by PCR using pAC5.1Sushi3EGFP as the template. The S3 gene was cloned into pBC vector by digestion with BbsI. After

multimerization, the clones containing 1, 2, 4 and 8 copies of S3 were selected (Figure 2a) and named pBCS3-1, -2, -4, -8mer, respectively. The *Nde*I and *Hind*III-flanking fragments of these clones were inserted into pET22b for expression of the multimeric S3 gene, and the expression levels were examined by SDS-PAGE. Of all the expression cassettes, the tetramer yielded the highest expression level, giving the expected recombinant S3 tetramer (rS3-4mer) of 18.4 kDa, which represented 25 % of the total cell proteins (Figure 2b). The monomer construct was not expression-competent, while the octamer construct expressed poorly.

The rS3-4mer was expressed as inclusion bodies in *E. coli*. The solubilization in 8 M urea and purification through Q-Sepharose anion exchange chromatography produced more than 95 % purity of rS3-4mer (Figure 2b), yielding 42 mg rS3-4mer per litre of culture. The purified protein was dialyzed and urea was removed gradually to allow the samples to refold. Dialysis also removed unspecific small molecular weight bacteria proteins, hence further improving the purity of the rS3-4mer. SDS-PAGE under non-reducing conditions showed majority of one band with the expected size (data not shown). A minor form of a larger aggregate was removed by size exclusion using Superose[®] 12 column (Pharmacia). The refolded protein was precipitated with 90 % ethanol and redissolved in acid digestion buffer to obtain the monomers (rS3-1mer). The process of acid digestion is time dependent. A one-day treatment yielded polymeric mixtures of four kinds of rS3 peptides: rS3-4, -3, -2, -1mer (Figure 3a). Within 2 days, more than 90 % of the multimers was cleaved to the monomers.

Recombinant Sushi3 peptides show stronger binding potency to LPS

Samples from the total cell proteins, purified rS3-4mer, partially digested rS3 polymers, rS3-1mer and
5 synthetic S3 peptide were resolved on tricine SDS-PAGE and subjected to Western analysis against anti-S3 antibody. The rS3-1mer and its partially digested polymeric repeats (2, 3 and 4mers) were immunoreactive to the polyclonal rabbit anti-S3 antibody (Figure 3b). Thus, the antibody can be
10 employed for the ELISA-based LPS binding assay.

ELISA-based LPS binding assay revealed different binding capabilities with rS3-1 mer, -4mer and synthetic S3. At 4 µg/ml, both recombinant peptides reached saturation of binding to LPS (Figure 4), while the synthetic peptide
15 continued linearly and required 20 µg/ml to reach saturation of binding with LPS (data not shown). The EBC₅₀ (Endotoxin Binding Concentration) of the peptide, which achieves 50 % of maximum binding to LPS on the ELISA plate, reflects the binding activity of peptide to LPS, with the lower EBC₅₀
20 indicating higher potency. The rS3-4mer, rS3-1mer and synthetic S3 peptides displayed EBC₅₀ at 0.41 µg/ml, 1.02 µg/ml and 9.74 µg/ml, respectively. The kinetics of binding of peptides to LPS in 20 mM Tris-Cl, pH7.3, was also measured by SPR analysis with BIAcore 2000 using HPA chip,
25 which was immobilized with LPS. The K_d values of synthetic S3, rS3-1mer and rS3-4mer are $(7.80 \pm 2.18) \times 10^{-7}$ M, $(4.74 \pm 2.34) \times 10^{-8}$ M, $(1.71 \pm 1.86) \times 10^{-8}$ M, respectively.

The recombinant S3 peptides inhibit endotoxin-induced LAL reaction and hTNF-α release from THP-1 cells

30 The 50 % endotoxin-neutralizing concentration (ENC₅₀) value of the peptides against 5 EU/ml of LPS was

determined to be 5.4 µg/ml for rS3-4mer, 9.2 µg/ml for rS3-1mer, and 10.2 µg/ml for synthetic S3 (Figure 5a). A lower ENC_{50} indicates higher potency of endotoxin neutralization. The binding isotherm of the two monomeric peptides, whether
5 it is recombinant or synthetic is similar, but rS3-4mer shows a 2-fold stronger LPS neutralization efficacy.

Similar results were also obtained by measuring the ability of rS3-4 & -1mer to inhibit LPS-induced hTNF- α production by THP-1 cells, which were incubated with 50
10 EU/ml of LPS containing various concentrations of peptides. As shown in Figure 5b, rS3-1mer required 83.2 µg/ml, whereas rS3-4mer required 40.4 µg/ml to achieve 50 % inhibition.

The peptides show minimal cytotoxicity to eukaryotic cells
15 Both recombinant peptides had minimal effect on cell permeabilization. At the highest concentration of 50 µM, only 2-3 % of cell lysis was caused by rS3-4mer, indicating that the recombinant multimers of S3 would have negligible contraindications, although the LPS binding
20 activity is amplified significantly.

(10) Recombinant sushi 3 peptides (rS3) labeled with quantum dot (QD) tags bacteria

rS3 purified from recombinant bacteria, was labeled with QD (referred to as QD-rS3) was used as a novel
25 fluorescent tag to detect the presence of bacteria. As an example to demonstrate the concept of specific tagging of certain bacteria by QD-rS3, experiments were carried out with 2 strains for gram negative bacteria (*Escherichia coli* and *Pseudomonas aeruginosa*) and a gram positive bacteria,
30 *Staphylococcus aureus*). By addition of small quantities of QD-rS3 to overnight cultures of the bacteria, one observes,

within minutes, the fluorescently labeled gram negative bacteria (which contain lipopolysaccharide, LPS to which rS3 specifically bind to) and no labeling of *S. aureus*. QD labeled rS3 is stable and emits strong fluorescence which readily biosenses the presence of gram negative bacteria.

This method can be applied to tagging bacteria in solution and in solid phase.

(11) *Covalent conjugation of rS3-4mer to DADPA-immobilized agarose beads*

10 rS3-4mer affinity matrix was prepared using DADPA-immobilized agarose. The peptide was dissolved in 1ml conjugation buffer [0.1M 2-(N-morpholino)ethanesulfonic acid (MES), pH 4.7] and used for conjugation by EDC, to DADPA-agarose packed in a column. After 3 hours of incubation, the
15 column was drained and washed with water. These eluents were collected in 1 ml fractions. The amount of peptide immobilized to the matrix was determined by measuring the absorbance of the fractions at 280nm.

20 Beads were regenerated with 10-column volumes of 1% DOC, followed by 10-column volumes of pyrogen-free water, 2 M NaCl and pyrogen-free water. When not in use, the peptide-conjugated beads were stored at 4°C with 0.02% sodium azide to prevent the growth of bacteria.

(12) *LPS adsorption assay*

25 After regeneration of the column and equilibration in the appropriate buffer, the LPS-binding capacity of rS3-4mer-coupled beads was tested batchwise. An aliquot of 5 ml of standard LPS solution (under different pH and in the presence or absence of chymotrypsinogen A and EDTA) was
30 allowed to flow through the column twice at room

temperature. Solutions before and after the treatment were collected to determine the LPS removal and protein recovery. EDTA was added in order to reduce the affinity of LPS to proteins. This helps to improve the removal of low levels of LPS from protein solutions. (Petsch 2000).

(13) Quantification of LPS and proteins

LPS was quantified by using the LAL chromogenic kinetic assay. The solutions were sonicated and diluted in borosilicate glass tubes at 37°C. Fifty µl of each mixture was carefully dispensed into appropriate wells of a sterile 96-well microtitre plate (Nuncclon™ Δ surface, Nunc). The reaction mixture was then incubated for 15 minutes at 37°C before 50µl of LAL reagent was added. The reaction mixtures were read at 405 nm every 5 minutes with a SPECTRAMax 340 plate reader running on SOFTmax PRO version 1.2.0. The temperature was kept at 37 °C during the incubation and measuring. Five LPS standards ranging from 0.005EU/ml to 50EU/ml were used to calibrate the absorbance into endotoxin concentration in EU/ml. A blank using pyrogen-free water and negative controls of only the peptides in buffer solution were also set up in the assay. All samples, blank, negative control and standards were in triplicates. Pyrogen-free water was used for dilution of reagents and peptides.

The protein concentration in sample solutions of before and after treatment was determined by measuring the absorbance at 280nm with a spectrophotometer DU 650 (Beckman).

(14) *Data analysis of LPS affinity studies**LPS affinity matrix preparation*

In preparing the rS3-4mer conjugated affinity matrix for LPS, 1.5 mg/ml of peptides was used for coupling.

- 5 1.27mg/ml of peptides was successfully coupled onto the affinity matrix with coupling efficiency of 87% achieved, based on the following calculations:

$$A_{280nm} \text{ before coupling (abs)} = 1.62$$

$$A_{280nm} \text{ of fraction recovery (abs)} = 0.0601 + 0.316 + 0.0472 +$$

10 $0.0204 + 0.0099 + 0.0033 + 0.0016 = 0.21$

$$\text{Total protein coupled on (abs)} = 1.62 - 0.21 = 1.41$$

$$\text{Coupling efficiency} = 1.41 / 1.62 = 87\%$$

15 *LPS binding by rS3-4mer affinity beads at various endotoxin concentrations*

- It is reported that the usual LPS problematic contamination level is up to 100EU/ml after the initial steps of purification. Thus, we tested the DADPA rS3-4mer and S3A column at these endotoxin concentrations. When
- 20 buffer solutions containing 20mM Tris-HCl, 100mM NaCl and 0.5M EDTA of pH7.3 were used, both spiked levels of 5 and 500 EU/ml. were reduced to below the detection limit of 0.005EU/ml for both the columns.

- However, LPS is normally found together with
- 25 proteins such as in pharmaceutical fluids. Therefore, there is a need to test the protein recovery and LPS removal under such conditions. There are electrostatic and hydrophilic interactions between proteins and LPS. These interactions

may reduce the efficiency of LPS removal. Very often, high protein recovery will compromise the removal of LPS from the solution and vice versa. In this work, 0.5mg/ml of chymotrypsinogen A was spiked into the same Tris buffer and
5 was passed through the column twice to test the ability of the conjugated agarose beads for selective removal of LPS from protein solutions.

For both the columns, the LPS-affinity beads were able to remove LPS to a concentration below the detection
10 limit of 0.005EU/ml. However, the rS3-4mer column appears to be able to recover more proteins compared to the S3A column under the current process conditions (Table 1).

Table 1
Removal of LPS from various solutions with problematic low levels of LPS contamination^a

Column	DADPA rS3\4mer				Protein recovery ^a (mg/ml)
	Tris buffer ^b (+EDTA) ^c			Chym. A ^b (+EDTA) ^c	
	LPS (EU/ml)				
Before treatment	5	50	100	50	0.5
After treatment	<0.005 ^d	<0.005 ^d	<0.005 ^d	<0.005 ^d	0.4175
Clearance factor (CF)	>1000	>10000	>20000	>10000	83.5% recovered

Column	DADPA S3A			Protein recovery ^a (mg/ml)
	Tris buffer ^b (+EDTA) ^c		Chym. A ^b (+EDTA) ^c	
	LPS (EU/ml)			
Before treatment	5	100		0.5
After treatment	<0.005 ^d	<0.005 ^d		0.3125
Clearance factor (CF)	>1000	>20000		62.5% recovered

5 ^a Aliquots of 5 ml of each sample solution containing LPS at indicated concentrations were passed through a column with 1ml of affinity beads. LPS concentration of samples was measured by LAL chromogenic assay.

^b Tris buffer: 20 mM Tris-HCl, pH 7.3 containing 100mM NaCl;

10 Chym. A: 0.5 mg/ml chymotrypsinogen A in same Tris buffer

^c EDTA at stock solution of 0.5 M (pH7.3) was added to the buffer to achieve a final concentration of 5mM before running through column.

^d 0.005EU/ml is the detection limit of LAL chromogenic assay.

15 ^e A_{280nm} intensity of the samples before and after treatment with beads were measured to calculate the protein recovery.

Characteristics of LPS binding by rS3-4mer affinity beads

20

To determine if the peptide is able to remove LPS under a wide range of pH, buffer solutions of different pH containing 100mM of NaCl were tested. Increase in pH was expected to cause electrostatic interaction between the negatively charged phosphate groups of LPS and the

25

positively charged peptides to weaken and decrease the binding capacity of the peptide (Ding et al. 2001).

We observe a significant drop in efficiency of LPS removal when the pH shifted from 5.0 to 6.0. This could be because pH of 6.0 is very near the isoelectric point of the rS3-4mer, peptide, thus causing the electrostatic interactions to weaken and hence, it loses its binding capacity for LPS. When the pH shifted from 6.0 to 7.3, the efficiency of these affinity beads was enhanced with clearance factor of more than 450. Further increase in pH causes the clearance factor to drop drastically to only 4.3, this maybe due to the increase of negative charge on peptide, so decrease the affinity of peptide to LPS, since the LPS is strongly negatively charged.

From the results, the rS3-4mer is able to remove LPS under a relatively wide range of pH, but with efficiencies highest only at around pH of 7.3 (Table 2).

Table 2

Removal of LPS from various solutions with problematic low levels of LPS contamination^a

Column	DADPA rS3\4mer				DADPA S3Δ
	Sodium acetate buffer ^b		Tris buffer ^c		
pH ^d	5.0	6.0	7.3	8.5	7.3
Before treatment (EU/ml)	500				
After treatment (EU/ml)	4.616	61.38	1.090	116.84	3.176
Clearance factor (CF)	108	8	459	4.3	157

^a Aliquots of 5 ml of each sample solution containing LPS at indicated concentrations were passed through a column with 1ml of affinity beads. LPS concentration of samples was measured by LAL chromogenic assay.

^b Sodium acetate buffer: 20 mM sodium acetate containing 100mM NaCl;

^c Tris buffer: 20 mM Tris-HCl containing 100mM NaCl;

^d pH adjusted to around 7 for LAL test by adding 5% of 1M Tris-HCl, pH7.3 for acidic samples and 4% 1M NaAc, pH5.0 for the pH8.5 sample.

- 5 ^e Clearance Factor (CF) which reflects the efficiency of LPS removal, is obtained by dividing concentration of LPS before with after treatment.

10 Removal of LPS in tissue culture medium

For the cell culture medium RPMI 1640, both columns were able to remove LPS from 120 EU/ml to below the detection limit of 0.005EU/ml.

15

Table 3

Removal of LPS from culture medium with problematic low level of LPS contamination^a

Column	Medium ^b	
	DADPA rS3\4mer	DADPA S3A
Before Treatment (EU/ml)	120	120
After treatment (EU/ml)	<0.005 ^c	<0.005 ^c
Clearance Factor (CF)	>24000	>24000

- 20 ^a Aliquots of 5 ml of each sample solution containing LPS at indicated concentrations were passed through a column with 1ml of affinity beads. LPS concentration of samples was measured by LAL chromogenic assay.

^b Medium: RPMI 1640 pH 9.0

^c 0.005EU/ml is the detection limit of LAL chromogenic assay.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- 5 (i) APPLICANT: Jeak L. DING; Bow HO; University of Singapore
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 10 (C) SOFTWARE: PatentIn Ver. 2.0
 (v) CURRENT APPLICATION DATA
 (A) APPLICATION NUMBER:
 (B) FILING DATE:

15 (2) INFORMATION FOR SEQ ID NO.: 1:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 34
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 20 (D) TOPOLOGY:
 (ii) MOLECULE TYPE: polypeptide
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Artificial Sequence
 (ix) FEATURE
 25 (C) OTHER INFORMATION: Sushi-3 peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1:

His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
 1 5 10 15

30 Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
 20 25 30

Leu Met

35

(2) INFORMATION FOR SEQ ID NO.: 2:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 34
 40 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY:
 (ii) MOLECULE TYPE: polypeptide
 (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: Artificial Sequence
 (ix) FEATURE
 (C) OTHER INFORMATION: Sushi-3delta peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2:

50 His Ala Glu His Lys Val Lys Ile Lys Val Lys Gln Lys Tyr Gly Gln
 1 5 10 15

55 Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
 20 25 30

Leu Met

41

(2) INFORMATION FOR SEQ ID NO.: 3:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 38

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: forward primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 3:

TCGAAGACGG CCCAGGATC CCCATGCTGA ACACAAGG 38

15

(2) INFORMATION FOR SEQ ID NO.: 4:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 35

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: reverse primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 4:

30 TAGAAGACCC GGGGGTCCAT CAAAGAAAGT AGTTA 35

WE CLAIM:

1. A polypeptide comprising a tetrameric repeat of
5 S3.
2. The polypeptide of claim 1 consisting of a tetrameric repeat of S3.
- 10 3. S3 peptide tagged with a detectable label.
4. The peptide of claim 3 wherein the label is detectable by fluorescence.
- 15 5. A method of producing the polypeptide of claim 1 or 2, comprising the steps of expressing a multimer of S3 in a host cell and cleaving the multimer of S3.
- 20 6. The method of claim 5 further comprising the step of isolating the polypeptide of claim 1 or 2 from S3 monomer or non-tetrameric S3.
7. The method of claim 5 or 6 wherein cleaving is by acid digestion.
- 25 8. The method of claim 5 or 6 wherein cleaving is by proteolytic digestion.
9. A method for detecting LPS-containing bacteria
30 comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide of claim 1 or 2, and detecting binding between LPS and the polypeptide of claim 1 or 2.

10. A method for detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide of claim 1 or 2, and detecting inhibition of LPS-induced activity.

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11. A method for treating endotoxaemia or sepsis comprising the step of administering the polypeptide of claim 1 or 2 to a patient suffering from endotoxaemia or sepsis.

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12. A method for detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide of claim 3, and detecting binding between LPS and the polypeptide of claim

15 3.

13. A method for detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide of claim 3, and detecting inhibition of LPS-induced activity.

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14. A method for detecting LPS-containing bacteria comprising the step of contacting a sample containing LPS-containing bacteria with the polypeptide of claim 4, and detecting bacteria-associated fluorescence from the label.

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15. The polypeptide of claim 1 or 2 or S3 peptide, immobilized on a solid medium.

16. The polypeptide of claim 15 wherein the solid medium is agarose bead.

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17. A method for removing LPS or LPS-containing
bacteria from a sample, comprising the step of contacting
the sample with the polypeptide of claim 15 or 16 under
conditions which allow binding of LPS-containing bacteria to
5 the polypeptide of claim 15 or 16, wherein unbound material
is substantially free of LPS or LPS-containing bacteria.

Fig. 1

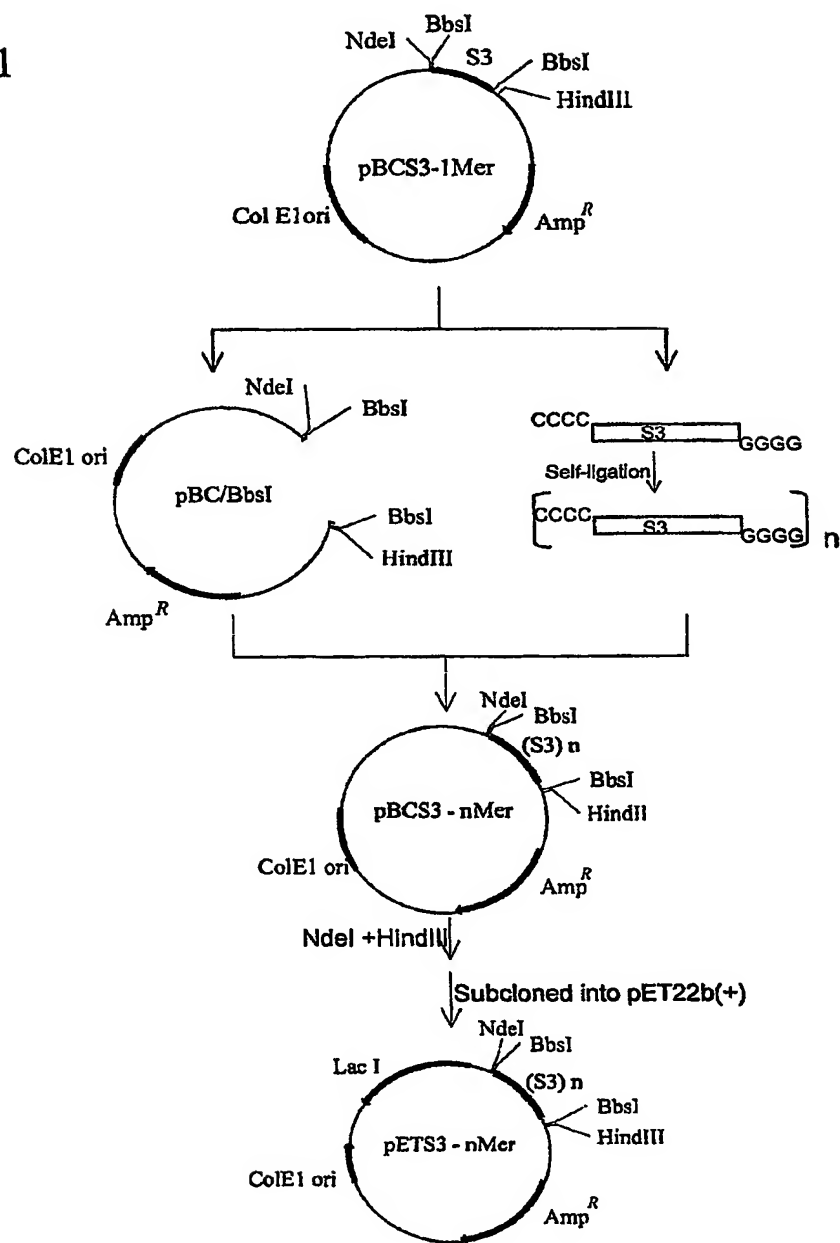
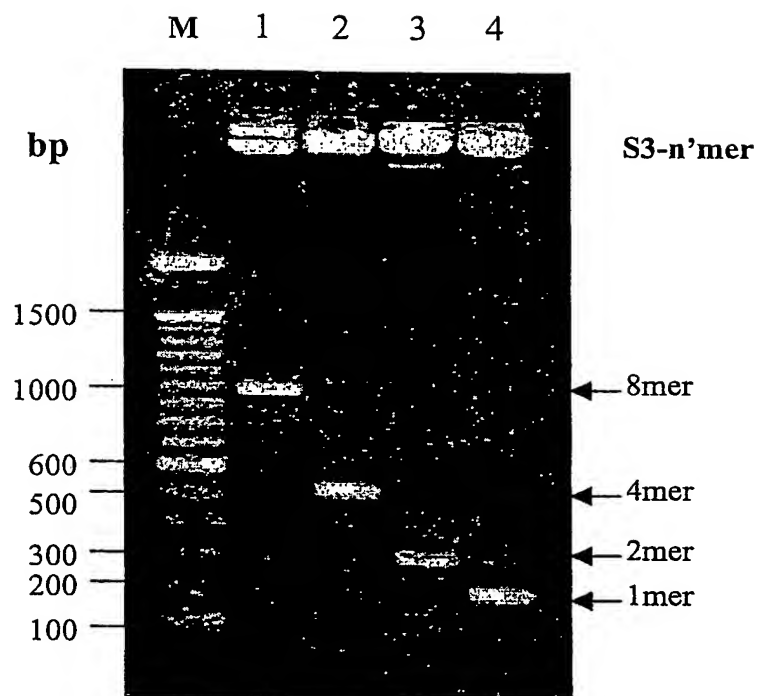


Fig. 2

(a)



(b)

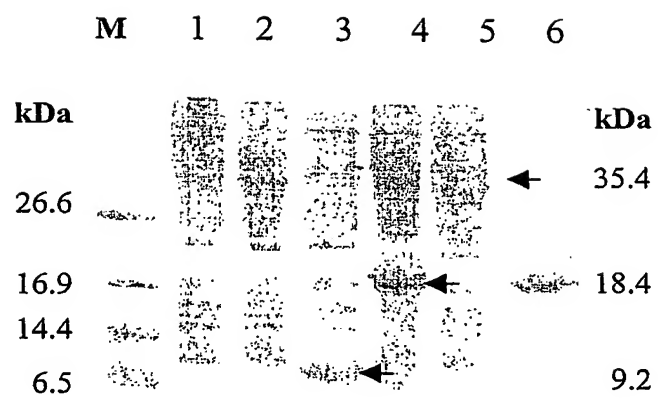
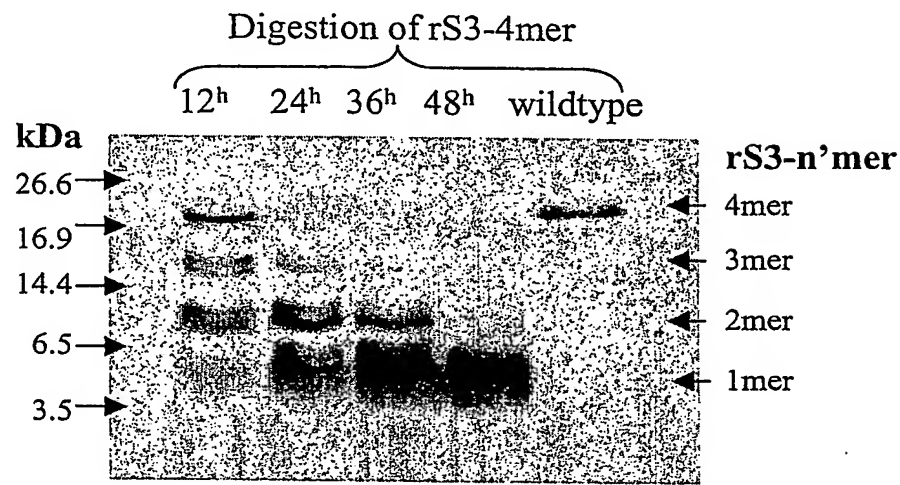


Fig. 3

(a)



(b)

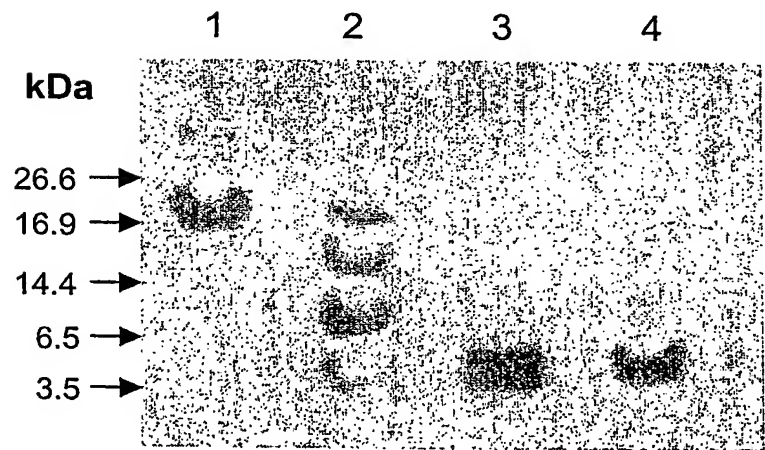


Fig. 4

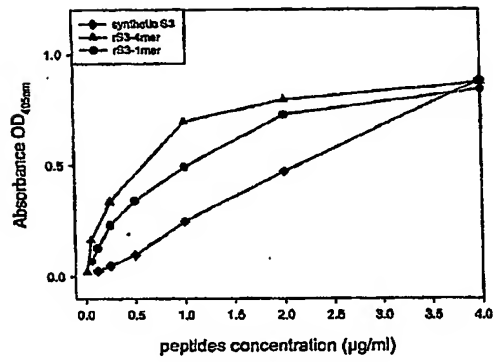


Fig. 5a

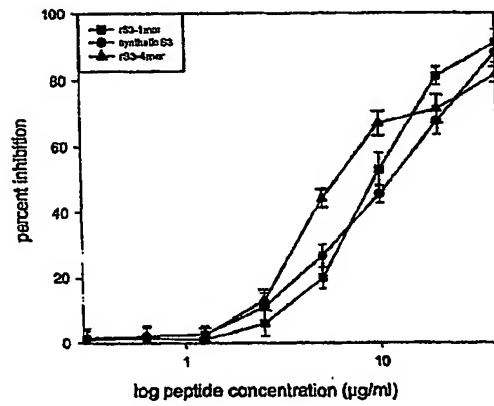


Fig. 5b

